

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/520,882
Source: PCF
Date Processed by STIC: 6/30/06

ENTERED



PCT

RAW SEQUENCE LISTING

DATE: 06/30/2006

PATENT APPLICATION: US/10/520,882

TIME: 08:37:14

Input Set : F:\403uspc.app.txt

Output Set: N:\CRF4\06302006\J520882.raw

3 <110> APPLICANT: Brumbley, Stevens Michael
 4 Purnell, Matthew Peter
 5 Chong, Barrie Fong
 6 Petrasovits, Lars Arved
 7 Nielsen, Lars Keld
 8 McQualter, Richard Bruce
 10 <120> TITLE OF INVENTION: TRANSGENIC PLANTS USED AS A BIOREACTOR SYSTEM
 12 <130> FILE REFERENCE: 900145.403USPC
 14 <140> CURRENT APPLICATION NUMBER: US 10/520,882
 C--> 15 <141> CURRENT FILING DATE: 2005-01-11
 17 <150> PRIOR APPLICATION NUMBER: PCT/AU2003/000903
 18 <151> PRIOR FILING DATE: 2003-07-11
 20 <150> PRIOR APPLICATION NUMBER: US 60/394,869
 21 <151> PRIOR FILING DATE: 2002-07-11
 23 <160> NUMBER OF SEQ ID NOS: 56
 25 <170> SOFTWARE: PatentIn version 3.0
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 1182
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Rastonia Eutropia
 32 <220> FEATURE:
 33 <221> NAME/KEY: CDS
 34 <222> LOCATION: (1)..(1182)
 36 <400> SEQUENCE: 1

37 atg act gac gtt gtc atc gta tcc gcc gcc cgc acc gcg gtc ggc aag	48
38 Met Thr Asp Val Ile Val Ser Ala Ala Arg Thr Ala Val Gly Lys	
39 1 5 10 15	
41 ttt ggc ggc tcg ctg gcc aag atc ccg gca ccg gaa ctg ggt gcc gtg	96
42 Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu Gly Ala Val	
43 20 25 30	
45 gtc atc aag gcc gcg ctg gag cgc gcc ggc gtc aag ccg gag cag gtg	144
46 Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro Glu Gln Val	
47 35 40 45	
49 agc gaa gtc atc atg ggc cag gtg ctg acc gcc ggt tcg ggc cag aac	192
50 Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn	
51 50 55 60	
53 ccc gca cgc cag gcc gcg atc aag gcc ggc ctg ccg gcg atg gtg ccg	240
54 Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro	
55 65 70 75 80	
57 gcc atg acc atc aac aag gtg tgc ggc tcg ggc ctg aag gcc gtg atg	288
58 Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met	
59 85 90 95	
61 ctg gcc gcc aac gcg atc atg gcg ggc gac gcc gag atc gtg gtg gcc	336

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62 Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala
63          100          105          110
65 ggc ggc cag gaa aac atg agc gcc gcc ccg cac gtg ctg ccg ggc tcg      384
66 Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser
67          115          120          125
69 cgc gat ggt ttc cgc atg ggc gat gcc aag ctg gtc gac acc atg atc      432
70 Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile
71          130          135          140
73 gtc gac ggc ctg tgg gac gtg tac aac cag tac cac atg ggc atc acc      480
74 Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr
75 145          150          155          160
77 gcc gag aac gtg gcc aag gaa tac ggc atc aca cgc gag gcg cag gat      528
78 Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp
79          165          170          175
81 gag ttc gcc gtc ggc tcg cag aac aag gcc gaa gcc gcg cag aag gcc      576
82 Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala
83          180          185          190
85 ggc aag ttt gac gaa gag atc gtc ccg gtg ctg atc ccg cag cgc aag      624
86 Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys
87          195          200          205
89 ggc gac ccg gtg gcc ttc aag acc gac gag ttc gtg cgc cag ggc gcc      672
90 Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala
91          210          215          220
93 acg ctg gac agc atg tcc ggc ctc aag ccc gcc ttc gac aag gcc ggc      720
94 Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly
95 225          230          235          240
97 acg gtg acc gcg gcc aac gcc tcg ggc ctg aac gac ggc gcc gcc gcg      768
98 Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala
99          245          250          255
101 gtg gtg gtg atg tcg gcg gcc aag gcc aag gaa ctg ggc ctg acc ccg      816
102 Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro
103          260          265          270
105 ctg gcc acg atc aag agc tat gcc aac gcc ggt gtc gat ccc aag gtg      864
106 Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val
107          275          280          285
109 atg gcc atg gcc ccg gtg ccg gcc tcc aag cgc gcc ctg tcg cgc gcc      912
110 Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu Ser Arg Ala
111          290          295          300
113 gag tgg acc ccg caa gac ctg gac ctg atg gag atc aac gag gcc ttt      960
114 Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe
115 305          310          315          320
117 gcc gcc cag gcg ctg gcg gtg cac cag cag atg ggc tgg gac acc tcc      1008
118 Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser
119          325          330          335
121 aag gtc aat gtg aac ggc ggc gcc atc gcc atc ggc cac ccg atc ggc      1056
122 Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly
123          340          345          350
125 gcg tcg ggc tgc cgt atc ctg gtg acg ctg ctg cac gag atg aag cgc      1104
126 Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg

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127          355          360          365
129 cgt gac gcg aag aag ggc ctg gcc tcg ctg tgc atc ggc ggc ggc atg      1152
130 Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met
131          370          375          380
133 ggc gtg gcg ctg gca gtc gag cgc aaa taa      1182
134 Gly Val Ala Leu Ala Val Glu Arg Lys
135 385          390
138 <210> SEQ ID NO: 2
139 <211> LENGTH: 393
140 <212> TYPE: PRT
141 <213> ORGANISM: Rastonia Eutropia
143 <400> SEQUENCE: 2
145 Met Thr Asp Val Val Ile Val Ser Ala Ala Arg Thr Ala Val Gly Lys
146 1          5          10          15
149 Phe Gly Gly Ser Leu Ala Lys Ile Pro Ala Pro Glu Leu Gly Ala Val
150          20          25          30
153 Val Ile Lys Ala Ala Leu Glu Arg Ala Gly Val Lys Pro Glu Gln Val
154          35          40          45
157 Ser Glu Val Ile Met Gly Gln Val Leu Thr Ala Gly Ser Gly Gln Asn
158          50          55          60
161 Pro Ala Arg Gln Ala Ala Ile Lys Ala Gly Leu Pro Ala Met Val Pro
162 65          70          75          80
165 Ala Met Thr Ile Asn Lys Val Cys Gly Ser Gly Leu Lys Ala Val Met
166          85          90          95
169 Leu Ala Ala Asn Ala Ile Met Ala Gly Asp Ala Glu Ile Val Val Ala
170          100          105          110
173 Gly Gly Gln Glu Asn Met Ser Ala Ala Pro His Val Leu Pro Gly Ser
174          115          120          125
177 Arg Asp Gly Phe Arg Met Gly Asp Ala Lys Leu Val Asp Thr Met Ile
178          130          135          140
181 Val Asp Gly Leu Trp Asp Val Tyr Asn Gln Tyr His Met Gly Ile Thr
182 145          150          155          160
185 Ala Glu Asn Val Ala Lys Glu Tyr Gly Ile Thr Arg Glu Ala Gln Asp
186          165          170          175
189 Glu Phe Ala Val Gly Ser Gln Asn Lys Ala Glu Ala Ala Gln Lys Ala
190          180          185          190
193 Gly Lys Phe Asp Glu Glu Ile Val Pro Val Leu Ile Pro Gln Arg Lys
194          195          200          205
197 Gly Asp Pro Val Ala Phe Lys Thr Asp Glu Phe Val Arg Gln Gly Ala
198          210          215          220
201 Thr Leu Asp Ser Met Ser Gly Leu Lys Pro Ala Phe Asp Lys Ala Gly
202 225          230          235          240
205 Thr Val Thr Ala Ala Asn Ala Ser Gly Leu Asn Asp Gly Ala Ala Ala
206          245          250          255
209 Val Val Val Met Ser Ala Ala Lys Ala Lys Glu Leu Gly Leu Thr Pro
210          260          265          270
213 Leu Ala Thr Ile Lys Ser Tyr Ala Asn Ala Gly Val Asp Pro Lys Val
214          275          280          285
217 Met Gly Met Gly Pro Val Pro Ala Ser Lys Arg Ala Leu Ser Arg Ala

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218      290      295      300
221 Glu Trp Thr Pro Gln Asp Leu Asp Leu Met Glu Ile Asn Glu Ala Phe
222 305      310      315      320
225 Ala Ala Gln Ala Leu Ala Val His Gln Gln Met Gly Trp Asp Thr Ser
226      325      330      335
229 Lys Val Asn Val Asn Gly Gly Ala Ile Ala Ile Gly His Pro Ile Gly
230      340      345      350
233 Ala Ser Gly Cys Arg Ile Leu Val Thr Leu Leu His Glu Met Lys Arg
234      355      360      365
237 Arg Asp Ala Lys Lys Gly Leu Ala Ser Leu Cys Ile Gly Gly Gly Met
238      370      375      380
241 Gly Val Ala Leu Ala Val Glu Arg Lys
242 385      390
245 <210> SEQ ID NO: 3
246 <211> LENGTH: 1280
247 <212> TYPE: DNA
248 <213> ORGANISM: Rastonia Eutropia
250 <400> SEQUENCE: 3
251 ggatccatga ctgacgttgt catcgtatcc gccgcccgca ccgcggtcgg caagtttggc      60
253 ggctcgctgg ccaagatccc ggcaccggaa ctgggtgccg tggcatcaa ggccgcgctg      120
255 gagcgcgccg gcgtcaagcc ggagcaggtg agcgaagtca tcatgggcca ggtgctgacc      180
257 gccggttcgg gccagaaccc cgcacgccag gccgcgatca aggccggcct gccggcgatg      240
259 gtgccggcca tgaccatcaa caaggtgtgc ggctcggggc tgaaggccgt gatgctggcc      300
261 gccaacgcga tcatggcggg cgacgccgag atcgtggtgg ccggcggcca ggaaaacatg      360
263 agcgccgccc cgcacgtgct gccgggctcg cgcgatggtt tccgatggg cgatgccaa      420
265 ctggtcgaca ccatgatcgt cgacggcctg tgggacgtgt acaaccagta ccacatgggc      480
267 atcaccgccc agaacgtggc caaggaatac ggcacacac gcgaggcgca ggatgagttc      540
269 gccgtcggtc cgcagaacaa ggccgaagcc gcgcagaagg ccggcaagtt tgacgaagag      600
271 atcgtcccgg tgctgatccc gcagcgcaag ggcgaccggg tggccttcaa gaccgacgag      660
273 ttcgtgcgcc agggcgccac gctggacagc atgtccggcc tcaagcccgc cttcgacaag      720
275 gccggcacgg tgaccgcggc caacgcctcg ggctgaacg acggcgccgc cgcggtggtg      780
277 gtgatgtcgg cggccaaggc caaggaactg ggctgacct cgctggccac gatcaagagc      840
279 tatgccaacg ccggtgtcga tcccaaggtg atgggcatgg gcccggtgcc ggcctccaag      900
281 cgcgccctgt cgcgcgccga gtggaccccg caagacctgg acctgatgga gatcaacgag      960
283 gcctttgccg cccaggcgct ggcggtgcac cagcagatgg gctgggacac ctccaaggtc      1020
285 aatgtgaacg gcggcgccat cgccatcggc caccgatcg gcgcgtcggg ctgccgtatc      1080
287 ctggtgacgc tgctgcacga gatgaagcgc cgtgacgcga agaagggcct ggctcgctg      1140
289 tgcacggcg gcggcatggg cgtggcgctg gcagtcgagc gcaaataagg aaggggtttt      1200
291 ccggggccgc gcgcggttgg cgcggaccgg gcgacgataa cgaagccaat caaggagtgg      1260
293 acatgactca ggggggtacc
296 <210> SEQ ID NO: 4
297 <211> LENGTH: 738
298 <212> TYPE: DNA
299 <213> ORGANISM: Rastonia Eutropia
301 <220> FEATURE:
302 <221> NAME/KEY: CDS
303 <222> LOCATION: (1)..(738)
305 <400> SEQUENCE: 4
306 atg act cag cgc att gcg tat gtg acc ggc ggc atg ggt ggt atc gga      48

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307 Met Thr Gln Arg Ile Ala Tyr Val Thr Gly Gly Met Gly Gly Ile Gly
308 1 5 10 15
310 acc gcc att tgc cag cgg ctg gcc aag gat ggc ttt cgt gtg gtg gcc 96
311 Thr Ala Ile Cys Gln Arg Leu Ala Lys Asp Gly Phe Arg Val Val Ala
312 20 25 30
314 ggt tgc ggc ccc aac tcg ccg cgc gaa aag tgg ctg gag cag cag 144
315 Gly Cys Gly Pro Asn Ser Pro Arg Arg Glu Lys Trp Leu Glu Gln Gln
316 35 40 45
318 aag gcc ctg ggc ttc gat ttc att gcc tcg gaa ggc aat gtg gct gac 192
319 Lys Ala Leu Gly Phe Asp Phe Ile Ala Ser Glu Gly Asn Val Ala Asp
320 50 55 60
322 tgg gac tcg acc aag acc gca ttc gac aag gtc aag tcc gag gtc ggc 240
323 Trp Asp Ser Thr Lys Thr Ala Phe Asp Lys Val Lys Ser Glu Val Gly
324 65 70 75 80
326 gag gtt gat gtg ctg atc aac aac gcc ggt atc acc cgc gac gtg gtg 288
327 Glu Val Asp Val Leu Ile Asn Asn Ala Gly Ile Thr Arg Asp Val Val
328 85 90 95
330 ttc cgc aag atg acc cgc gcc gac tgg gat gcg gtg atc gac acc aac 336
331 Phe Arg Lys Met Thr Arg Ala Asp Trp Asp Ala Val Ile Asp Thr Asn
332 100 105 110
334 ctg acc tcg ctg ttc aac gtc acc aag cag gtg atc gac ggc atg gcc 384
335 Leu Thr Ser Leu Phe Asn Val Thr Lys Gln Val Ile Asp Gly Met Ala
336 115 120 125
338 gac cgt ggc tgg ggc cgc atc gtc aac atc tcg tcg gtg aac ggg cag 432
339 Asp Arg Gly Trp Gly Arg Ile Val Asn Ile Ser Ser Val Asn Gly Gln
340 130 135 140
342 aag ggc cag ttc ggc cag acc aac tac tcc acc gcc aag gcc ggc ctg 480
343 Lys Gly Gln Phe Gly Gln Thr Asn Tyr Ser Thr Ala Lys Ala Gly Leu
344 145 150 155 160
346 cat ggc ttc acc atg gca ctg gcg cag gaa gtg gcg acc aag ggc gtg 528
347 His Gly Phe Thr Met Ala Leu Ala Gln Glu Val Ala Thr Lys Gly Val
348 165 170 175
350 acc gtc aac acg gtc tct ccg ggc tat atc gcc acc gac atg gtc aag 576
351 Thr Val Asn Thr Val Ser Pro Gly Tyr Ile Ala Thr Asp Met Val Lys
352 180 185 190
354 gcg atc cgc cag gac gtg ctc gac aag atc gtc gcg acg atc ccg gtc 624
355 Ala Ile Arg Gln Asp Val Leu Asp Lys Ile Val Ala Thr Ile Pro Val
356 195 200 205
358 aag cgc ctg ggc ctg cca gaa gag atc gcc tcg atc tgc gcc tgg ttg 672
359 Lys Arg Leu Gly Leu Pro Glu Glu Ile Ala Ser Ile Cys Ala Trp Leu
360 210 215 220
362 tcg tcg gag gag tcc ggt ttc tcg acc ggc gcc gac ttc tcg ctc aac 720
363 Ser Ser Glu Glu Ser Gly Phe Ser Thr Gly Ala Asp Phe Ser Leu Asn
364 225 230 235 240
366 ggc ggc ctg cat atg ggc 738
367 Gly Gly Leu His Met Gly
368 245
371 <210> SEQ ID NO: 5
372 <211> LENGTH: 246

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/520,882

DATE: 06/30/2006
TIME: 08:37:15

Input Set : F:\403uspc.app.txt
Output Set: N:\CRF4\06302006\J520882.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:34; N Pos. 1,2,3,4,5,6
Seq#:35; N Pos. 1,2,3,4,5,6
Seq#:36; N Pos. 1,2,3,4,5,6
Seq#:37; N Pos. 1,2,3,4,5,6
Seq#:41; N Pos. 1,2,3,4,5,6
Seq#:42; N Pos. 1,2,3,4,5,6
Seq#:43; N Pos. 1,2,3,4,5,6
Seq#:48; N Pos. 1,2
Seq#:49; N Pos. 1,2

VERIFICATION SUMMARY

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Input Set : F:\403uspc.app.txt

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L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3408 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3413 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:34
L:3414 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0
L:3424 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3428 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:35
L:3429 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:35 after pos.:0
L:3439 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3443 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:36
L:3444 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:36 after pos.:0
L:3454 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3458 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:37
L:3459 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37 after pos.:0
L:3502 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3506 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:41
L:3507 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:0
L:3517 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3521 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:42
L:3522 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:42 after pos.:0
L:3532 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3536 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:43
L:3537 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:43 after pos.:0
L:3591 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3595 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:48
L:3596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:48 after pos.:0
L:3606 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:3610 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:49
L:3611 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0